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Fig. 1A.

-43 ATACTGGCTCAACCTCGGAGCTCACACTCAGGCTGGGGGCC

-26 Met Gly Arg Arg Val Pro Ala Leu Arg Gln Leu Val Leu Ala Val Leu Leu Leu Lys Pro Ser Gln Leu Gln  
 1 ATG GGG CGG CGA GTC CCA GCT CTG AGA CAG CTG CTG GTG GCA GTG CTG CTG CTG CTG AAG CCT TCA CAG CTG CAG

-1 Ser Arg Glu Leu Ser Gly Ser Arg Cys Pro Glu Pro Cys Asp Cys Ala Pro Asp Gly Ala Leu Arg Cys Pro Gly  
 76 TCC CGA GAG CTG TCA GGG TCG TCG GAG CCC GAG TGC TGC GAC TGC GCA CCG GAT GGC GGC TGT CCT GGC

25 Pro Arg Ala Gly Leu Ala Arg Leu Ser Leu Thr Tyr Leu Pro Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly  
 151 CCT CGA GCC GGC CTC GCA CTA TCT CTC ACC TAT CTC CCT GTC AAA GTA ATT CCA TCA CAA GCT TTC AGG GGA

50 Leu Asn Glu Val Val Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn  
 226 CTT AAT GAG GTC GTA AAA ATT GAA ATC TCT CAG AGT GAT TCC CTG GAA AGG ATA GAA GCT AAT GCC TTT GAC AAC

75 Leu Leu Asn Leu Ser Glu Leu Leu Ile Gln Asn Thr Lys Asn Leu Tyr Ile Glu Pro Gly Ala Phe Thr Asn  
 301 CTC CTC AAT TTG TCT GAA CTA CTG ATC CAG AAC ACC AAA AAC CTG CTA TAC ATT GAA CCT GCT TTT ACA AAC

100 Leu Pro Arg Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly Ile Arg Thr Leu Pro Asp Val Thr Lys Ile Ser Ser  
 376 CTC CCT CGG TTA AAA TAC CTG AGC ATC TGT AAC ACA GGC ATC CGA ACC CTT CCA GAT GTT ACG AAG ATC TCC TCC

125 Ser Glu Phe Asn Phe Ile Leu Glu Ile Cys Asp Asn Leu His Ile Thr Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly  
 451 TCT GAA TTT AAT TTC ATT CTG GAA ATC TGT GAT AAC TTA CAC ATA ACC ACC ATA CCC GGG AAT GCT TTC CAA GGG

150 Met Asn Asn Glu Ser Val Thr Leu Lys Leu Tyr Gly Asn Gly Phe Glu Glu Val Gln Ser His Ala Phe Asn Gly  
 526 ATG AAT AAC GAG TCT GTC ACA CTA AAA CTG TAT GGA AAT GGA TTT GAA GAA GTA CAA AGC CAT GCA TTC AAT GGG

175 Thr Thr Leu Ile Ser Leu Glu Leu Lys Glu Asn Ile Tyr Leu Leu Glu Lys Met His Ser Ser Gly Ala Phe Gln Gly Ala  
 601 ACG ACT CTA ATC TCG CTG GAG CTA AAA GAA GAA AAC ATC TAC CTG GAG AAG ATG CAC AGT GGA GCC TTC CAG GGG GCC

200 Thr Gly Pro Ser Ile Leu Asp Ile Ser Ser Thr Lys Leu Gln Ala Leu Pro Ser His Gly Leu Glu Ser Ile Gln  
 676 ACG GGG CCC AGC ATC CTG GAT ATT TCT TCC ACC AAA TTG CAG GCC CTG CCG AGC CAC GGG CTG GAG TCC ATT CAG

225 Thr Leu Ile Ala Leu Ser Tyr Ser Leu Lys Thr Leu Pro Ser Lys Glu Lys Phe Thr Ser Leu Leu Val Ala  
 751 ACG CTC ATC GCC CTG TCT TCC TAC TCA CTG AAA ACA CTG CCC TCC AAA GAA AAA TTC ACG AGC CTC CTG GTC GCC

250 Thr Leu Thr Tyr Pro Ser His Cys Cys Ala Phe Arg Asn Leu Pro Lys Lys Glu Gln Asn Phe Ser Phe Ser Ile  
 826 ACG CTG ACC TAC CCC AGC CAC TGC TGC GCC TTT CCG AAG AAA GAA GAA CAG AAT TTT TCA TTT TCC ATT

275 Phe Glu Asn Phe Ser Lys Gln Cys Glu Ser Thr Val Arg Lys Ala Asp Asn Glu Thr Leu Tyr Ser Ala Ile Phe  
 901 TTT GAA AAC TTC TCC AAA CAA TGC GAA AGC ACA GTT AGA AAA GCA GAT AAC GAG ACG CTT TAT TCC GCC ATC TTT

Fig. 1B.

300 Glu Glu Asn Glu Ser Gly Trp Asp Tyr Asp Tyr Gly Phe Cys Ser Pro Lys Thr Leu Gln Cys Ala Pro Glu  
976 GAG GAG AAT GAA CTC AGT AGT GGC TGG GAT TAT GAT TAT GGC TTC TGT TCA CCC AAG ACA CTC CAA TGT GCT CCA GAA

325 Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Ala Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile  
1051 CCA GAT GCT TTC AAC CCC TGT GAA GAT ATT ATG GGC TAT GCC TTC CTT AGG GTC CTG ATT TGG CTG ATT AAT ATA

350 Leu Ala Ile Phe Gly Asn Leu Thr Val Leu Phe Val Leu Leu Thr Ser Arg Tyr Lys Leu Thr Val Pro Arg Phe  
1126 CTA GCC ATC TTT GGC AAC CTG ACA GTC CTC TTT GTT CTC CTG ACC AGT CGT TAT AAA CTG ACA GTG CCC CGC TTC

375 Leu Met Cys Asn Leu Ser Phe Ala Asp Phe Cys Met Gly Leu Tyr Leu Leu Ile Ala Ser Val Asp Ser Gln  
1201 CTC ATG TGT AAT CTC TCC TTT GCA GAC TTT TGC ATG GGC CTC TAC CTG CTC ATT GCC TCC GTG GAC TCC CAA

400 Thr Lys Gly Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys Gly Ala Ala Gly Phe Phe Thr  
1276 ACA AAA GGC CAG TAC TAT AAC CAC GCC ATA GAC TGG CAG ACA GGG AGT GGC TGC GGT GCA GCT GGC TTC TTT ACT

425 Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala  
1351 GTG TTT GCC AGT GAA CTC TCT GTC TAC ACC CTG ACG GTT ATC ACC CTG GAA AGG TGG CAC ACC ATC ACC TAT GCT

450 Val Gln Leu Asp Gln Lys Leu Arg Leu Arg His Ala Ile Pro Ile Met Leu Gly Gly Trp Leu Phe Ser Thr Leu  
1426 GTA CAG CTA GAC CAA AAG CTA AGA CTG AGA CTG AGG CAT GCC ATC CCA ATT ATG CTC GGA GGA TGG CTC TTT TCT ACG CTG

475 Ile Ala Thr Met Pro Leu Val Gly Ile Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met Asp Val Glu Ser  
1501 ATC GCC ACG ATG ATG CCC CTT GTG GGT ATC AGC AAT TAC ATG AAG GTC AGC ATC TGC CTC CCC ATG GAT GTG GAA TCC

500 Thr Leu Ser Gln Val Tyr Ile Leu Ser Ile Leu Asn Val Val Ala Phe Val Val Ile Cys Ala Cys Tyr  
1576 ACT CTG TCC CAA GTC TAC ATA TTA TCC ATC CTC AAC GTG GTG GCC TTC GTC GTC ATC TGT GCT TGC TAC

525 Ile Arg Ile Tyr Phe Ala Val Gln Asn Pro Glu Leu Thr Ala Pro Asn Lys Asp Thr Lys Ile Ala Lys Lys Met  
1651 ATT AGG ATC TAC TTT GCA GTT CAA AAT CCA GAG CTG ACA GCT CCT AAC AAG GAC ACA AAA ATT GCT AAG AAG ATG

Fig. 1C.

550 Ala Ile Leu Ile Phe Thr Asp Phe Thr Cys Met Ala Pro Ile Ser Phe Phe Ala Ile Ser Ala Ala Phe Lys Val  
 1726 GCC ATC CTC ATC TTC ACA GAC TTC ACG TGC ATG GCG CCC ATC TCT TTC TTT GCC ATC TCG GCT GCC TTC AAA GTG

575 Pro Leu Ile Thr Val Thr Asn Ser Lys Ile Leu Leu Val Leu Phe Thr Tyr Pro Val Asn Ser Cys Ala Asn Pro Phe  
 1801 CCC CTT ATC ACT GTC ACC AAC TCG AAA ATC TTA CTG GTC CTT TTT TAT CTT GTC AAT TCT TGT GCC AAT CCA TTT

600 Leu Tyr Ala Ile Phe Thr Lys Ala Phe Gln Arg Asp Phe Leu Leu Leu Ser Arg Phe Gly Cys Cys Lys Arg  
 1876 CTG TAT GCG ATC TTC ACG AAG GCG TTT CAG AGA GAT TTC CTT CTG CTG AGC CGA TTC GGC TGC TGT AAA CGC

625 Arg Ala Glu Leu Tyr Arg Arg Lys Glu Phe Ser Ala Tyr Thr Ser Asn Cys Lys Asn Gly Phe Pro Gly Ala Ser  
 1951 CGG GCG GAG CTT TAC AGA AGG AAG GAA TTT TCT GCA TAT ACT TCC AAC TGC AAA AAT GGC TTC CCA GGA GCA AGT

650 Lys Pro Ser Gln Ala Thr Leu Lys Leu Ser Thr Val His Cys Gln Pro Ile Pro Arg Ala Leu Thr His  
 2026 AAG CCG TCC CAG GCT ACC CTG AAG TTG TCC ACA GTG CAC TGT CAA CAG CCC ATA CCA CCG AGA GCG TTA ACT CAC

2101 TAGCATTACAAAATTTGGCCTAAATATGTTTTTAAAGAGTGTTTTAGAAAATATTTATCCTTAGGCACCTTCAGGAGAAATGTACCTGCTCAGAGGAC  
 2201 GGCCATAACACACTTGGTCACATAAGTTTCAGGAAGTTTAGAAATTTTATAGTAATTTAGGCATAAATATTTTGTGAATCTAATACTAAGGAATC  
 2301 TAAGTTGTCAATTTTCAGCTCTCGACATTTTTCATTTCAATCTTGTGATTACATTTGTAATCTCCAAATATATTTACTTCATAGCAGATTGAAAATTTAA  
 2401 ACTGGTCTTTGCTCAGATAGTTTGATAAATATATTCAAGAGATGCACTGTGAGTGTGACTGCTAGCCTTGCATGGTAAATAGAGTTTCTTAGCCAT  
 2501 ATTCCAAGTGTCTCACATGTACACATGAGGAGGACAGATGCAAACTGTTTACATCAGTGAATCTATTAGCCAGCTCTATTCTAGAGACTTCTATTCCC  
 2601 ATTGACACTCTGCTTAATCTTCCATCTGAAGGCACATGCTGCATATTTGTTGGCTTACAGATCAGTACCTCATGGCCAGGAGCCCATCTCAGCCCA  
 2701 TCTTGTCTCTCTATCTCAGGATCTTGGAAATGCTACACAGCAAGCATGCCCTAGCCAGTTAACTCCCTAAATCTACACAGGAAAATATTTCTACCCAC  
 2801 CTTAGCATATTGTTTTCGATGATTACATGCTTCTGTATTTTGCCCTCCTCTAGTATC

3/2

1hrk	<u>KELSGSRKPEPNDFAPD</u> GALXXPGP	1hrf	(M) X (S) <u>GAFQ</u> GATGPSILD PV	(E)	(I)
1hrr	(M) XXESVTLKLYGNCFEEVQ				
1hr28	(K) NLLYIEPGSF	1hrc	(M) (D) YA (G) LXVLI (G) LINILD XF	(G) (F)	(F)
				(A)	
1hr26	(K) XYGNXFEXVQ			(N)	

Fig. 2A.

		TM-1																				TM-2																													
LH/CGR	339	F	L	R	V	L	I	W	L	I	N	I	L	A	I	F	G	N	L	T	V	L	F	V	L	L	T	S	-	-	R	Y	K	L	-	T	V	P	R	F	L	M	C	N	L	S	F	A	D	F	384
RHO	36	Q	F	S	M	L	A	A	Y	M	F	L	L	I	M	L	G	F	P	I	N	F	L	T	L	Y	V	T	V	Q	H	K	K	L	R	T	P	L	N	Y	I	L	L	N	L	A	V	A	D	L	84
SKR	35	L	W	T	A	A	Y	L	A	L	V	L	V	A	V	M	G	N	A	T	V	I	W	I	L	A	-	-	-	H	Q	R	M	R	T	V	T	N	Y	F	I	V	N	L	A	L	A	D	L	80	
B-2AR	35	G	M	G	I	V	M	S	L	I	V	L	A	I	V	F	G	N	V	L	V	I	T	A	I	A	K	-	-	-	F	E	R	L	Q	T	V	T	N	Y	F	I	T	S	L	A	C	A	D	L	80
5HT-2R	53	W	S	A	L	L	T	T	V	V	I	L	T	I	A	G	N	I	L	V	I	M	A	V	S	L	-	-	-	E	K	K	L	Q	N	A	T	N	Y	F	L	M	S	L	A	I	A	D	M	99	

4/2

	TM-3																																																			
LH/CGR	C	M	G	L	Y	L	L	I	A	S	V	D	S	Q	T	K	G	Q	Y	N	H	A	I	D	W	Q	T	G	-	S	G	C	G	A	A	G	F	F	T	V	F	A	S	E	L	S	V	Y	433			
RHO	F	M	V	F	G	G	F	T	T	L	Y	T	S	L	-	-	-	-	-	-	-	-	-	H	G	Y	F	V	F	G	P	T	G	C	N	L	E	G	F	F	A	T	L	G	G	E	I	A	L	W	126	
SKR	C	M	A	A	F	N	A	A	F	N	F	V	Y	A	S	-	-	-	-	-	-	-	-	H	N	I	W	Y	F	G	R	A	F	C	Y	F	Q	N	L	F	P	I	T	A	M	F	V	S	I	Y	122	
B-2AR	V	M	G	L	A	V	V	P	F	G	A	A	H	I	L	-	-	-	-	-	-	-	-	M	K	M	W	T	F	G	N	F	W	C	E	F	W	T	S	I	D	V	L	C	V	T	A	S	I	E	122	
5HT-2R	L	L	G	F	L	V	M	P	V	S	M	L	T	I	L	-	-	-	-	-	-	-	-	Y	G	Y	R	W	P	L	P	S	K	L	C	A	I	W	I	Y	L	D	V	L	F	S	T	A	S	I	M	142

	TM-4																																																		
LH/CGR	T	L	T	V	I	T	L	E	R	W	H	T	I	T	Y	A	V	Q	L	D	Q	K	L	R	L	R	H	A	I	P	I	M	L	G	G	W	L	F	S	T	L	I	A	T	M	P	L	V	G	I	483
RHO	S	L	V	V	L	A	I	E	R	Y	V	V	V	C	K	P	M	S	N	F	R	F	-	G	E	N	H	A	I	M	G	V	A	F	T	W	V	M	A	L	A	C	A	A	P	P	L	V	G	W	175
SKR	S	M	T	A	I	A	A	D	R	Y	M	A	I	V	H	P	F	Q	P	R	L	S	A	P	G	T	R	A	-	-	V	I	A	G	I	W	L	V	A	L	A	L	A	F	-	P	Q	C	F	Y	169
B-2AR	T	L	C	V	I	A	V	D	R	Y	F	A	I	T	S	P	F	K	Y	Q	S	L	L	T	K	N	K	A	R	V	I	I	L	M	V	W	I	V	S	G	L	T	S	F	L	P	I	Q	M	H	172
5HT-2R	H	L	C	A	I	S	L	D	R	Y	V	A	I	Q	N	P	I	H	H	S	R	F	N	S	R	T	K	A	F	L	K	I	I	A	V	W	T	I	S	V	G	I	S	M	-	P	I	P	V	F	191

Fig. 2B.

TM-5

LH/CGR	S	N	Y	-	-	-	M	K	V	S	I	C	L	P	M	D	V	E	S	T	L	-	-	-	S	Q	V	Y	I	L	S	I	L	I	L	N	V	V	A	F	-	V	V	I	C	A	C	Y	I	R	526	
RHO	S	R	Y	I	P	E	G	M	Q	C	S	C	G	I	D	Y	Y	T	P	H	E	E	T	N	N	E	S	F	V	I	Y	M	F	V	V	H	F	I	I	P	L	I	V	I	F	F	C	Y	G	Q	225	
SKR	S	T	I	T	D	E	G	A	T	K	C	V	V	A	W	P	E	D	S	G	G	K	M	L	L	L	Y	H	L	I	V	I	A	L	I	Y	F	L	P	L	V	V	M	F	V	A	Y	S	V	219		
β-2AR	W	Y	R	A	T	H	Q	E	A	I	N	C	Y	A	N	E	T	C	C	D	F	-	F	T	N	Q	A	Y	A	I	A	S	S	I	V	S	F	Y	V	P	L	V	I	M	V	F	V	Y	S	R	221	
5HT-2R	G	L	Q	D	D	S	K	V	F	K	E	G	S	C	L	L	A	D	-	-	-	-	-	-	-	-	D	N	F	V	L	I	G	S	F	V	A	F	F	I	P	L	T	I	M	V	I	T	Y	F	L	234

TM-6

LH/CGR	I	Y	F	A	V	Q	N	P	E	L	T	A	P	N	K	D	T	K	I	A	K	K	M	A	I	L	I	F	T	D	F	T	-	C	M	A	P	I	S	F	F	A	I	S	A	A	F	K	V	P	575
RHO	L	V	F	T	V	K	E	A	A	A	(8)	Q	K	A	E	K	E	V	T	R	M	V	I	I	M	V	I	A	F	L	I	C	W	L	P	Y	A	G	V	A	F	Y	I	F	T	H	Q	G	280		
SKR	I	G	L	T	L	W	R	R	S	V	(12)	L	Q	A	K	K	F	V	K	T	M	V	L	V	V	T	F	A	I	C	W	L	P	Y	H	L	Y	F	I	L	G	T	F	Q	E	D	278				
β-2AR	V	F	Q	E	A	K	R	Q	L	Q	(33)	C	L	K	E	H	K	A	L	K	T	L	G	I	I	M	G	T	F	T	L	C	W	L	P	F	F	I	V	N	I	V	H	V	I	Q	D	N	301		
5HT-2R	T	I	K	S	L	Q	K	E	A	T	(48)	I	S	N	E	Q	K	A	C	K	V	L	G	I	V	F	F	L	F	V	V	M	W	C	P	F	F	I	T	N	I	M	A	V	I	C	K	E	329		

TM-7

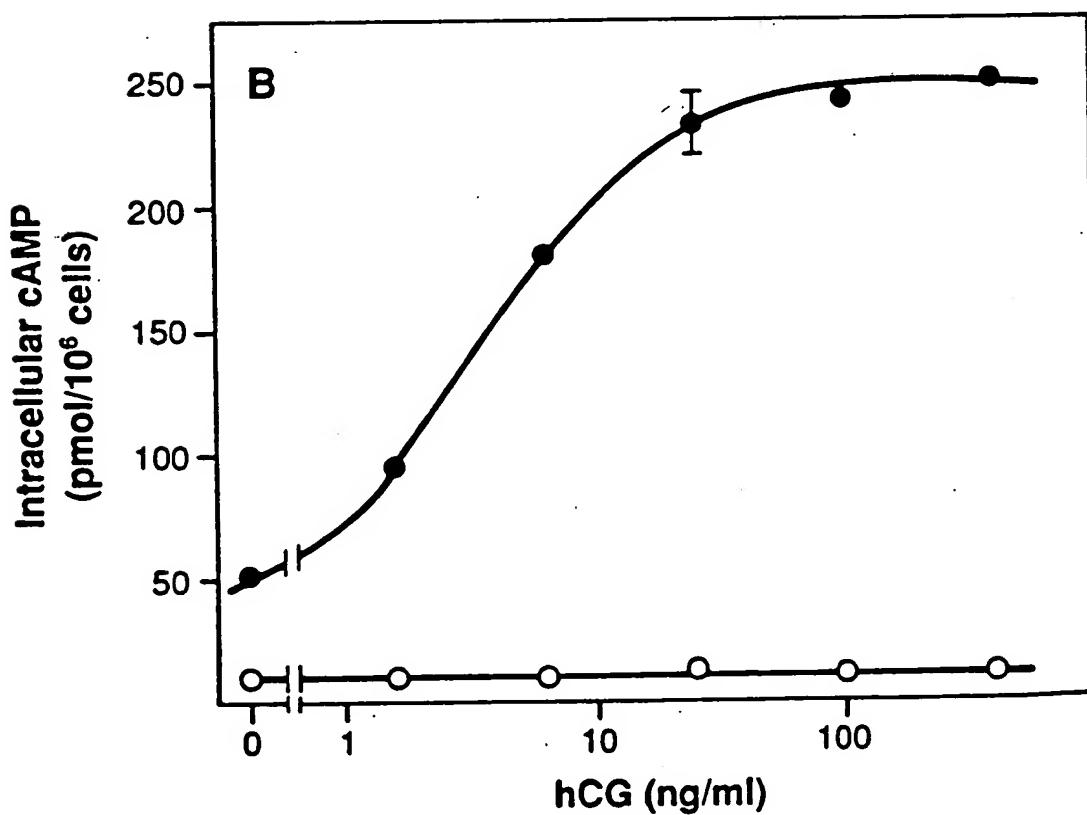
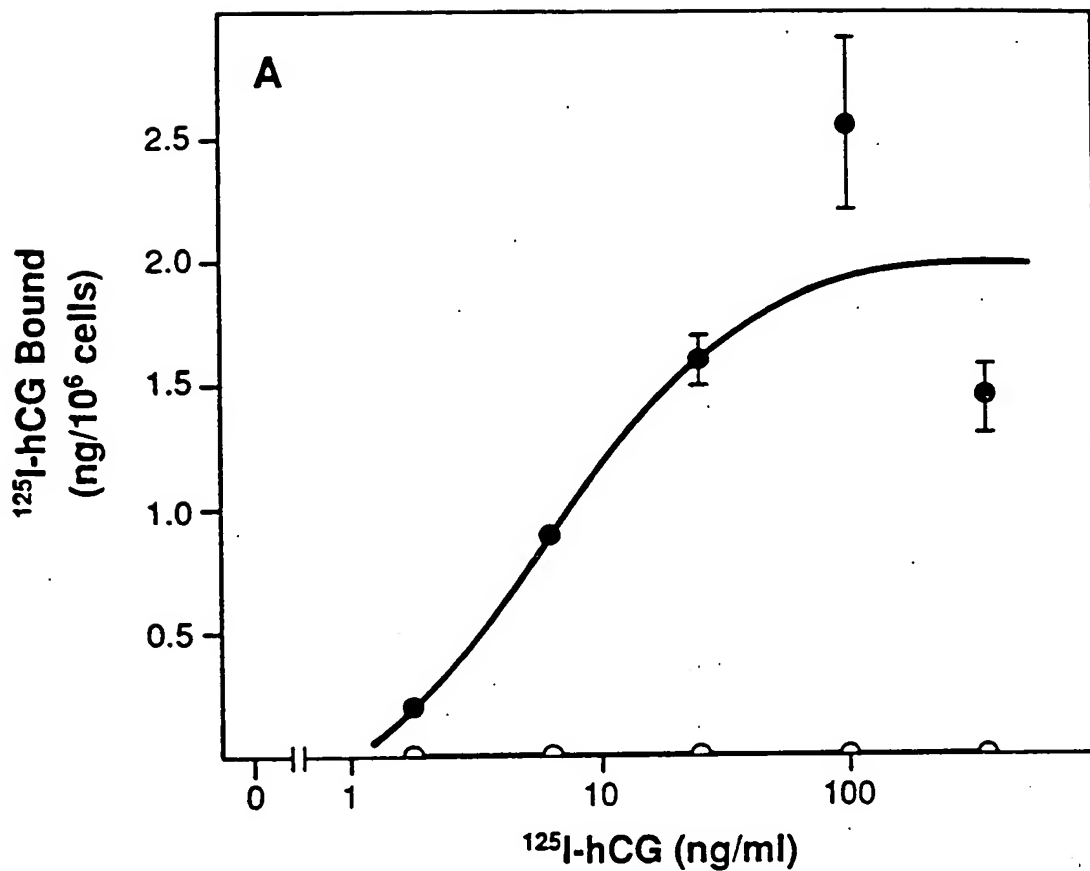
LH/CGR	L	I	T	V	T	N	S	-	-	-	K	I	L	L	V	L	F	Y	P	V	N	S	C	A	N	P	F	L	Y	A	I	F	T	K	A	F	Q	R	D	F	L	L	L	S	R	F	G	C	621/674	
RHO	S	D	F	G	P	I	F	-	-	-	M	T	I	P	A	F	F	A	K	T	S	A	V	Y	N	P	V	I	Y	I	M	M	N	K	Q	F	R	N	C	M	V	T	T	L	C	G	K	N	326/348	
SKR	I	Y	C	H	K	F	I	Q	Q	-	Y	L	A	L	F	W	L	A	M	S	S	T	M	Y	N	P	I	I	Y	C	C	L	N	H	R	F	R	S	G	F	R	L	A	F	R	C	P	W	327/384	
β-2AR	L	I	R	K	E	V	-	-	-	Y	I	L	L	N	W	I	G	Y	V	N	S	G	F	N	P	L	I	Y	-	C	R	S	P	D	F	R	I	A	F	Q	E	L	L	C	L	R	R	S	345/413	
5HT-2R	S	C	N	E	N	V	I	G	A	L	L	N	V	F	V	W	I	G	Y	L	S	S	A	V	N	P	L	V	Y	T	L	F	N	K	T	Y	R	S	A	F	S	R	Y	I	Q	C	Q	Y	K	378/449

**B**

LRG	L	x	L	P	x	-	-	L	x	x	L	x	-	x	L	D	L	S	x	N	x						
Toll	L	x	x	L	P	x	x	-	-	L	F	x	H	x	x	N	L	x	-	x	L	x	x	N	x		
GPIB	L	T	T	L	P	x	G	-	-	L	L	x	x	L	P	x	L	x	-	x	L	x	L	S	x	N	x
ACY	a	x	x	a	P	x	x	-	-	-	a	x	x	L	x	x	L	x	-	x	L	x	L	x	x	N	x

7/12

Fig. 4.



8/12

*Fig. 5.*



Fig. 6A.

-71	AGGAGCCTGG	GGAATCTGTG	GAAGTTTTTCG	CGCTGATGCA	GAAAGAAAGT	CGGTGAAATGG				
-10	ATAAATAAGG	ATG GCC	TTG CTC	CTG GTC	TCC TTG	CTG GCA	TTC TTG	GGC ACG	GGA TCT	GGA
-17		Met Ala	Leu Leu	Leu Val	Ser Leu	Leu Ala	Phe Leu	Gly Thr	Gly Ser	Gly
51	TGT CAT	CAC TGG	CTG TGT	CAT TGC	TCT AAT	AGG GTC	TTT CTC	TGC CAA	GAC AGC	AGG
1	Cys His	His Trp	Leu Cys	His Cys	Ser Asn	Arg Val	Phe Leu	Cys Gln	Asp Ser	Lys
111	ACA GAG	ATT CCG	ACC GAC	CTC CCC	CGG AAC	GCC ATT	GAA CTG	AGG TTT	GTG CTC	ACC
21	Thr Glu	Ile Pro	Thr Asp	Leu Pro	Arg Ala	Ile Glu	Leu Arg	Phe Val	Leu Thr	Lys
171	CTT CGA	GTC ATC	CCG AAA	GGA TCA	TTT GCT	GGA TTT	GGA GAC	CTG GAG	AAA ATA	GAG
41	Leu Arg	Val Ile	Pro Lys	Gly Ser	Phe Ala	Gly Phe	Gly Asp	Leu Glu	Lys Ile	Glu
231	TCT CAG	AAT GAT	GTC TTG	GAA GTA	ATA GAG	GCA GAT	GTG TTC	TCC AAC	CTA CCC	AAG
61	Ser Gln	Asn Asp	Val Leu	Glu Val	Ile Glu	Ala Asp	Val Phe	Ser Asn	Leu Pro	Lys
291	CAT GAA	ATT AGG	ATT GAA	AAG GCC	AAC AAT	CTT CTG	TAC ATC	AAC CCG	GAG GCC	TTC
81	His Glu	Ile Arg	Ile Glu	Lys Ala	Asn Asn	Leu Leu	Tyr Ile	Asn Pro	Glu Ala	Phe
351	AAT CTC	CCC AGT	CTC AGA	TAT CTG	TTA ATA	TCC AAC	ACA GGC	ATT AAG	CAC TTG	CCA
101	Asn Leu	Pro Ser	Leu Arg	Tyr Leu	Leu Ile	Ser Asn	Thr Gly	Ile Lys	His Leu	Pro
411	GTT CAC	AAG ATC	CAG TCT	CTC CAA	AAG GTT	CTA CTA	GAC ATT	CAA GAT	AAC ATA	AAC
121	Val His	Lys Ile	Gln Ser	Leu Gln	Lys Val	Leu Leu	Asp Ile	Gln Asp	Asn Ile	Asn
471	CAC ATC	GTT GCC	AGG AAC	TCC TTC	ATG GGA	CTG AGT	TTT GAA	AGT GTG	ATT TTA	TGG
141	His Ile	Val Ala	Arg Asn	Ser Phe	Met Gly	Leu Ser	Phe Glu	Ser Val	Ile Leu	Trp
531	AGT AAG	AAT GGG	ATT GAA	GAA ATA	CAC AAC	TGT GCA	TTC AAC	GGA ACT	CAG CTA	GAT
161	Ser Lys	Asn Gly	Ile Glu	Glu Ile	His Asn	Cys Ala	Phe Asn	Gly Thr	Gln Leu	Asp
591	CTG AAT	CTA AGC	GAT AAC	AAT TTT	GAA GAA	TTG CCT	CCT AAT	GAC GTT	TTC CAG	GGA
181	Leu Asn	Leu Ser	Asp Asn	Asn Asn	Leu Glu	Glu Leu	Pro Asn	Val Phe	Gln Gly	Ala
651	TCT GGG	CCA GTC	ATT TTA	GAT ATC	TCA AGG	ACA AAG	GTC CAT	TCC TTA	CCA AAC	CAT
201	Ser Gly	Pro Val	Ile Leu	Asp Ile	Ser Arg	Thr Lys	Val His	Ser Leu	Pro Asn	His
711	TTA GAA	AAT CTG	AAG AAG	CTG AGG	GCC TCA	ACA TAC	CGC TTG	AAA AAG	CTC CCT	AAT
221	Leu Glu	Asn Leu	Lys Lys	Arg Ala	Arg Ser	Thr Tyr	Arg Leu	Lys Lys	Leu Pro	Asn
771	CTG GAC	AAG TTT	GTC ACC	CTC ATG	GAG GCC	AGC CTC	ACC TAC	CCC AGC	CAC TGC	TGT
241	Leu Asp	Lys Phe	Val Thr	Leu Met	Glu Ala	Ser Leu	Thr Tyr	Pro Ser	His Cys	Cys
831	TTT GCA	AAC TTG	AAG CCG	CAA ATC	TCT GAA	CTT CAT	CCA ATT	TGC AAC	AAG TCT	ATT
261	Phe Ala	Asn Leu	Lys Arg	Gln Ile	Ser Glu	Leu His	Pro Ile	Cys Asn	Lys Ser	Ile
891	AGG CAA	GAT ATT	GAT ATG	ACT CAA	ATT GGG	GAT CAG	AGA GTC	TCT CTG	ATA GAT	GAT
281	Arg Gln	Asp Ile	Asp Asp	Met Thr	Gln Ile	Gly Asp	Gln Arg	Val Ser	Leu Ile	Asp
951	GAA CCC	AGT TAT	GGA AAA	GGA TCT	GAC ATG	ATG TAC	AAT GAA	TTT GAT	TAT GAC	TTA
301	Glu Pro	Ser Tyr	Gly Lys	Gly Ser	Asp Met	Met Tyr	Asn Glu	Phe Asp	Tyr Asp	Leu
1011	AAT GAA	GTT GTT	GAT GTG	ACC TGC	TCA CCA	AAG CCA	GAT GCA	TTT AAT	CCA TGT	GAA
321	Asn Glu	Val Val	Asp Val	Thr Cys	Ser Pro	Lys Pro	Ala Phe	Asn Pro	Cys Glu	Asp

Fig. 6B.

1071	ATC	ATG	GGG	TAC	AAC	ATC	CTC	AGG	GTC	TTG	ATA	TGG	TTT	ATT	AGC	ATC	CTG	GCC	ATT	ACT
341	Ile	Met	Gly	Tyr	Asn	Ile	Leu	Arg	Val	Leu	Ile	Trp	Phe	Ile	Ser	Ile	Leu	Ala	Ile	Thr
1131	GGG	AAG	ACC	ACA	GTG	CTG	GTG	GTC	CTG	ACC	ACA	AGC	CAA	TAC	AAA	CTA	ACT	GTG	CCC	CGG
361	Gly	Asn	Thr	Thr	Val	Leu	Val	Val	Leu	Thr	Thr	Ser	Gln	Tyr	Lys	Leu	Thr	Val	Pro	Arg
1191	TTT	CTT	ATG	TGT	AAC	CTC	GCC	TTC	GCT	GAT	CTC	TGC	ATA	GGC	ATC	TAC	TTG	CTA	CTT	ATA
381	Phe	Leu	Met	Cys	Asn	Leu	Ala	Phe	Ala	Asp	Leu	Cys	Ile	Gly	Ile	Tyr	Leu	Leu	Ile	Ile
1251	GCA	TCA	GTT	GAC	ATC	CAT	ACC	AAG	AGC	CAG	TAC	CAC	AAC	TAT	GCC	ATT	GAC	TGG	CAA	ACA
401	Ala	Ser	Val	Asp	Ile	His	Thr	Lys	Ser	Gln	Tyr	His	Asn	Tyr	Ala	Ile	Asp	Trp	Gln	Thr
1311	GGA	GCA	GGC	TGT	GAT	GCT	GCT	GGC	TTT	TTC	ACT	GTC	TTT	GCC	AGT	GAA	CTG	TCA	GTC	TAC
421	Gly	Ala	Gly	Cys	Asp	Ala	Ala	Gly	Phe	Phe	Thr	Val	Phe	Ala	Ser	Glu	Leu	Ser	Val	Tyr
1371	ACA	TTG	ACA	GCC	ATC	ACC	CTA	GAA	AGA	TGG	CAT	ACC	ATC	ACA	CAT	GCT	ATG	CAA	CTG	GAA
441	Thr	Leu	Thr	Ala	Ile	Thr	Leu	Glu	Arg	Trp	His	Thr	Ile	Thr	His	Ala	Met	Gln	Leu	Glu
1431	TGC	AAG	GTG	CAG	CTC	CGG	CAT	GCT	GCC	AGC	GTC	ATG	GTA	TTG	GGC	TGG	ACT	TTT	GCC	TTC
461	Cys	Lys	Val	Gln	Leu	Arg	His	Ala	Ala	Ser	Val	Met	Val	Leu	Gly	Trp	Thr	Phe	Ala	Phe
1491	GCA	GCT	GCT	CTC	TTC	CCC	ATC	TTT	GGC	ATC	AGT	AGC	TAC	ATG	AAA	GTG	AGC	ATC	TGC	CTG
481	Ala	Ala	Ala	Leu	Phe	Pro	Ile	Phe	Gly	Ile	Ser	Ser	Tyr	Met	Lys	Val	Ser	Ile	Cys	Leu
1551	CCC	ATG	GAT	ATC	GAC	AGC	CCT	TTG	TCA	CAG	CTG	TAT	GTT	ATG	GCC	CTC	CTT	GTC	CTC	AAT
501	Pro	Met	Asp	Ile	Asp	Ser	Pro	Leu	Ser	Gln	Leu	Tyr	Val	Met	Ala	Leu	Leu	Val	Leu	Asn
1611	GTC	CTG	GCC	TTT	GTG	GTC	ATC	TGT	GGC	TGC	TAT	ACC	CAC	ATC	TAC	CTC	ACA	GTG	AGG	AAT
521	Val	Leu	Ala	Phe	Val	Val	Ile	Cys	Gly	Cys	Tyr	Thr	His	Ile	Tyr	Leu	Thr	Val	Arg	Asn
1671	CCT	ACC	ATT	GTG	TCC	TCA	TCA	AGC	GAC	ACC	AAG	ATT	GCC	AAG	CGC	ATG	GCC	ACA	CTC	ATC
541	Pro	Thr	Ile	Val	Ser	Ser	Ser	Ser	Asp	Thr	Lys	Ile	Ala	Lys	Arg	Met	Ala	Thr	Leu	Ile
1731	TTC	ACA	GAC	TTT	CTC	TGC	ATG	GCC	CCC	ATT	TCA	TTT	GCC	ATT	TCT	GCC	TCC	CTC	AAG	Lys
561	Phe	Thr	Asp	Phe	Leu	Cys	Met	Ala	Pro	Ile	Ser	Phe	Phe	Ala	Ile	Ser	Ala	Ser	Leu	Lys
1791	GTG	CCG	CTC	ATC	ACT	GTG	TCC	AAG	GCC	AAG	ATT	CTC	CTA	GTT	CTG	TTT	TAC	CCC	ATC	AAT
581	Val	Pro	Leu	Ile	Thr	Val	Val	Ser	Lys	Ala	Lys	Ile	Leu	Leu	Val	Phe	Tyr	Pro	Ile	Asn
1851	TCT	TGT	GCC	AAT	CCT	TTC	CTC	TAC	GCC	ATT	TTC	ACC	AAG	AAC	TTC	CGC	AGG	GAC	TTC	TTC
601	Ser	Cys	Ala	Asn	Pro	Phe	Leu	Tyr	Ala	Ile	Phe	Thr	Lys	Asn	Phe	Arg	Arg	Asp	Phe	Phe
1911	ATC	CTG	CTG	AGC	AAG	TTT	GGC	TGT	TAT	GAA	ATG	CAA	GCC	CAG	ATT	TAC	AGG	ACA	GAA	ACC
621	Ile	Leu	Leu	Ser	Lys	Phe	Gly	Cys	Tyr	Glu	Met	Gln	Ala	Gln	Ile	Tyr	Arg	Thr	Glu	Thr
1971	TCA	TCC	GCT	ACC	CAC	AAC	TTC	CAT	GCC	CGA	AAG	AGC	CAC	TGC	TCC	TCA	GCT	CCC	AGA	GTC
641	Ser	Ser	Ala	Thr	His	Asn	Phe	His	Ala	Arg	Lys	Ser	His	Cys	Ser	Ser	Ala	Pro	Arg	Val
2031	ACC	AAT	AGT	TAC	GTG	CTT	GTC	CCT	CTT	AAT	CAT	TCA	TCC	CAG	AAC	TAA	TAATCA	TGTGAAAA		
661	Thr	Asn	Ser	Tyr	Val	Leu	Val	Pro	Leu	Asn	His	Ser	Ser	Gln	Asn					
2094	TG	GATCCTCACC	TTGAAAGACA	ATTATGACTC	CTTCTGAAGA	GCAGGCCCATG	GACTAAATGG	CAATCCTACT												
2166	GCACATCTCA	TCTAATTTAA	TCTCTCTGGG	TCTCTGATG	GCAGACTGAT	CAGGGACCAT	TAATCACCCC													
2236	TTTGGCTCCT	CTCACACTTA	AATAATGGTA	ACAGCAATA	AAACAAGCA	AAACCGACA														

See also 6, 7 (mutual)

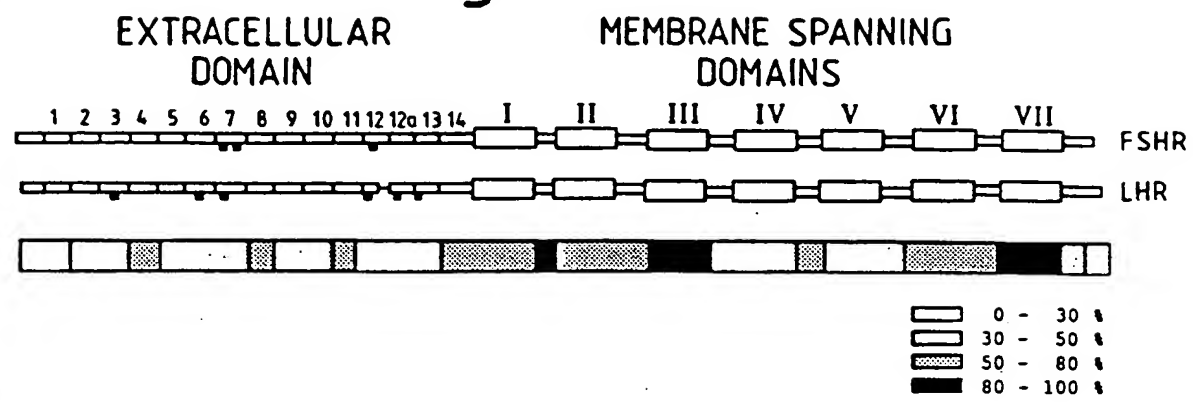
← See also 5

10/2

11/12

Fig.7.

A)



B)

1 RELSGSR PE.F D APDGA R PGPRAGLAR..... SLTYLFVK  
 1 CHHWLCHCSNRVFL.CQDSKVTETDLP RNAIELRFVLTQLR

41 SQA R LNEVV S S R NA D LN S LL QNTK  
 43 VIPKGSFAGFGDLEKIEISQNDVLEVIEADVFSNLPKLHEIRIEKANLL

91 E G T R K S C RT D T S SEFNFI E C LH T  
 91 YINPEAFQNLPSRLRYLLISNTGIKHLPAVHKIQSLQ.KVLLDIQDNINIH

141 TIPG A Q MNN T K YG F VQSH T IS E KE IY K  
 142 IVARNSFMGLSFESVILWLSKNQIEIHNCAFNGTQDELNLSDNNNLEE

191 MHSGA T S S LQA S SIQT I L S S T SK  
 192 LPNDVFQGASGPVILDISRTKVHSLPNHGLENLKKLRARSTYRLKKLPNL

241 E TS LV T R PKKE.....QNFSSIFENFSKQC  
 242 DKFVTLMEASLTYP SHCCAFANLKRQISELHPICNKSILRQIDDMTQIG

283 EST RKA N TL SAIFEENELSGWDY GF S.PKTLQ A E  
 292 DQRVSIIDDEPSYG...KGSDDMYNEFDYDLCEVVDVTCSPKPDFAFNPC

TM I

332 AF LN F L F L R S  
 339 EDIMGYNILRVLIWFISILAITGNTTVLVLTTSQYKLTVPFLMCNLAF

TM II TM III

382 F M L SQ G Y H S G  
 389 ADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCAAGFTVFASELS

TM IV

432 V Y V DQ LR IPI LG L STLI TM LV  
 439 VYTLTAITIERWHTITHAMQLECKVQLRHAASVMVLGWTFFAAAALFPIF

TM V

482 N VE T V ILSI I V A IR FA  
 489 GISSYMKVSICLPMDIDSPLSLYVMALLVLNVLAFFVICGCYTHIYLTV

TM VI

532 Q ELTAPNK K I T AF TN  
 539 RNPTIVSSSSDTKIAKFMATLIFTDFLCMAPISSFFAISASLVPLITVSK

TM VII

582 S V A Q  
 589 AKILLVLFYPINSCANPFLYAIFTNERRDE T

631 ..... EF.. YTSNCKNGFPGI I  
 639 ETSSATHNFHARKSHCSSAPRVNTNSYVLVPI .

693 PPRALTH rat LH/CG recept r seq #3  
 639 ..... rat FSH r cept r seq #7

12/12

Fig.8.

	(1- 19)	C	H	H	W	L	C	H	C	S	N	R	V	F	L	C	Q	-	-	D	S	K									
1	(20- 40)	V	T	E	I	P	T	D	L	P	R	N	A	I	E	L	R	F	V	-	L	T	K								
2	(41- 66)	L	R	V	I	P	K	G	S	F	A	G	F	G	D	L	E	K	I	E	I	S	Q	N	D	V					
3	(67- 90)	L	E	V	I	E	A	D	V	F	S	N	L	P	K	L	H	E	I	R	I	E	K	A	N	N					
4	(91-114)	L	L	Y	I	N	P	E	A	F	Q	N	L	P	S	L	R	Y	L	L	I	S	-	N	T	G					
5	(115-139)	I	K	H	L	P	A	V	H	K	I	Q	S	L	Q	K	V	L	L	D	I	Q	D	N	I	N					
6	(140-164)	I	H	I	V	A	R	N	S	F	M	G	L	S	F	E	S	V	I	L	W	L	S	K	N	G					
7	(165-188)	I	E	E	I	H	N	C	A	F	G	T	Q	L	D	E	L	-	L	S	D	N	N	N	N						
8	(189-212)	L	E	E	L	P	N	D	V	F	Q	G	A	S	G	P	V	I	L	D	I	S	R	T	K						
9	(213-234)	V	H	S	L	P	N	H	G	L	E	N	L	K	K	L	R	A	R	S	T	Y	R								
10	(235-251)	L	K	K	L	P	N	L	D	K	F	V	T	L	M	E	A	S													
11	(252-283)	L	T	Y	P	S	H	C	A	F	A	N	L	K	R	Q	I	S	E	L	H	P	I	C	K	S	I	L	R	Q	D
12	(284-297)	I	D	D	M	T	Q	I	G	D	Q	R	V	S	L																
13	(298-325)	I	D	D	E	P	S	Y	G	K	G	S	D	M	M	Y	N	E	F	D	Y	D	L	C	N	E	V	V	D		
14	(326-348)	V	T	C	S	P	K	P	D	A	F	N	P	C	E	D	I	M	G	Y	N	I	L	R							

Fig.9.

